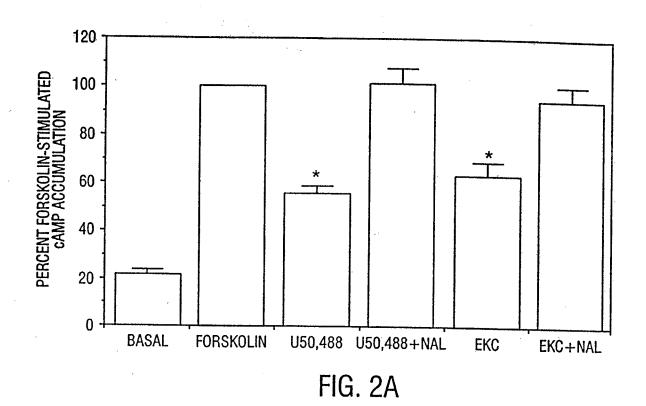
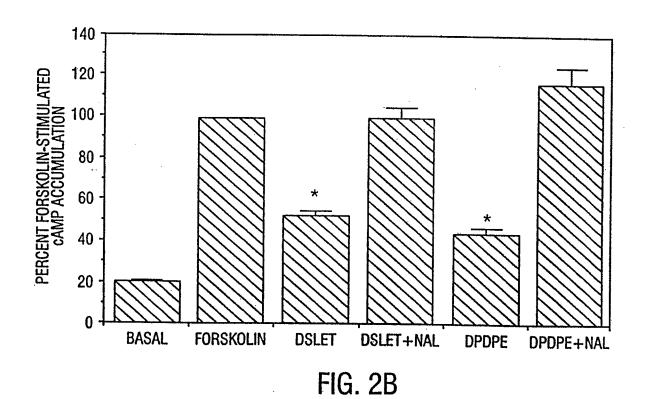
	IWI	
mORK1	morki mespiqifradpaptcspsacllp <u>n</u> sssw::::::Fpnwaesds <u>n</u> gsvasedqqlesahispaipviitavy	99
mord1	MORD1 ME::::::::::::LVPSARAELQSSPLVNLSDAFPSAFPSAGANASGSPGARSASSL:::ALAIAITALY	26
mork1	<pre>mORK1 SVVFVVGLVGNSLVMFVIIRYTKMKTATNIYIFNLALADALVTTTMPFQSAVYLMNSWPFGDVLCKIVISID 1 * * *** ** **** * **** ***********</pre>	138
mORD1		128
mORK1	<pre>mORK1 YYNMFTSIFTLTMMSVDRYIAVCHPVKALDFRTPLKAKIINICIWLLASSVGISAIVLGGTKVREDVDVIEC 2 ************************************</pre>	210
mORD1	<pre>MORD1 YYNMFTSIFTLTMMSVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVGVPIMVMAVTQPRDGAVV::C 1 TM 5</pre>	198
mORK1	PVLIIIVCYTLMILRLKSVRLLSGSREKDRNLRRITKLVLVVVAV	282
MORD1	MORD1 MLQFPSPSW:YWDTVTKICVFLFAFVVPILIITVCYGLMLLRLRSVRLLSGSKEKDRSLRRITRMVLVVVGA 2 TM 6	569
mORK1	<pre>mORK1 FIICWTPIHIFILVEALGSTSHSTAALSSYY:FCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRME 3 * ** ***** * *</pre>	353
mord1	MORDI FVVCWAPIHIFVIVWTLVDINRRDPLVVAALHLCIALGYANSSLNPVLYAFLDENFKRCFRQLCRTPCGRQE 3	341
MORK1	<pre>mORK1 RQSTNRVRNTVQDP::::ASMRDVGGMNKPV 380 (SEQ ID NO:2)</pre>	•
mORD1	MORD1 PGSLRRPRQATTRERVTACTPSDGPGGGAAA 372 (SEQ ID NO:4)	٠

FIG. 1





	AAGAAGCAAAATCAGTAATCCAAAGGCTATCACAAACACATTCACCTTATGGGGTTTGAC
61	TyrThrLysMetLysThrAla TTGAAAATGGAGGGAAATGCTATTGTTTCTTTTAGATACACAAGATGAAGACAG
121	ThrAsnIleTyrIlePheAsnLeuAlaLeuAlaAspAlaLeuValThrThrThrMetPro CAACCAACATTTACATATTTAACCTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGC
181	PheGlnSerThrValTyrLeuMetAsnSerTrpProPheGlyAspValLeuCysLysIle CCTTTCAGAGTACGGTCTACTTGATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGA
241	ValileSerIleAspTyrTyrAsnMetPheThrSerIlePheThrLeuThrMetMetSer TAGTAATTTCCATTGATTACTACAACATGTTCACCAGCATCTTCACCTTGACCATGATGA
301	ValAspArgTyrIleAlaValCysHisProValLysAlaLeuAspPheArgThrProLeu GCGTGGACCGCTACATTGCCGTGTGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCT
361	LysAlaLysIleIleAsnIleCysIleTrpLeuLeuSerSerValGlyIleSerAla TGAAGGCAAAGATCATCAATATCTGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTG

361	LysAlaLysIleIleAsnIleCysIleTrpLeuLeuSerSerValGlyIleSerAla TGAAGGCAAAGATCATCAATATCTGCATCTGGCTGCTGTCGTCATCTGGCATCTCTG
421	IleValLeuGlyGlyThrLysValArgGluA CAATAGTCCTTGGAGGCACCAAAGTCAGGGAAGGT::::::::::
. 481	spValAspValIleGluCysCysLeuGlnPheProAsp GGTTTTTATTGCCCTCCTCCAGACGTCGATGTCATTGAGTGCTGCTTGCAGTTCCCAGAT
541	AspAspTyrSerTrpTrpAspLeuPheMetLysIleCysValPheIlePheAlaPheVal GATGACTACTCCTGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTG
601	IleProValLeuIleIleIleValCysTyrThrLeuMetIleLeuArgLeuLysNNNVal ATCCCTGTCCTCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGANNGTC
661	ArgLeuLeuSerGlySerArgGluLysAspNNNAsnLeuArgArgIleThrArgLeuVal

FIG. 3B

. 661	ArgLeuLeuSerGlySerArgGluLysAspNNNAsnLeuArgArgIleThrArgLeuVal CGGCTCCTTTCTGGCTCCCGAGAGAAGATNNCAACCTGCGTAGGATCACCAGACTGGTC	
721	LeuValValValAlaValPheValValCysTrpThrProIleHisIlePheIleLeuVal CTGGTGGTGGTGGCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCTGGTG	
781	GluAlaLeuGlySerThrSerHisSerThrAlaAlaLeuSerSerTyrTyrPheCysIle GAGGCTCTGGGGAGCACCTCCCACAGCACAGCTGCTCTCCCAGCTATTACTTCTGCATC	
841	AlaLeuGlyTyrThrAsnSerSerLeuAsnProIleLeuTyrAlaPheLeuAspGluAsn GCCTTAGGCTATACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAAC	
901	PheLysArgCysPheArgAspPheCysPheProLeuLysMetNNNMetGluArgNNNSer TTCAAGCGGTGTTTCCGGGACTTCTGCTTTCCACTGAAGATGAGNATGGAGCGCNAGAGC	
961	ThrSerArgValArgAsnThrValGlnAspProAlaTyrLeuArgGluIleAspGlyMet ACTAGCAGAGTCCGAAATACAGTTCAGGATCCTGCTTACCTGAGGGAGATCGATGGGATG	
1021	MetAsnLysProValop ATGAATAAACCAGTATGACTAGTCGTGGA (SEQ ID NO:11)	
	FIG. 3C	

11e 11e

Thr /

Ala Ala

Thr

Lys Lys

Tyr Thr Lys Met L Tyr Thr Lys Met L 90

Asn Asn 95

Cys	Asn	Gln	Ala	Va1 80
Thr 15	Pro	Gln	Thr	ren -
Ser Pro Ile Gln Ile Phe Arg Gly Asp Pro Gly Pro Thr Cys 5 15	Ser Ala Cys Leu Leu Pro Asn Ser Ser Ser Trp Phe Pro Asn 20	Glu Ser Asp Ser Asn Gly Ser Val Gly Ser Glu Asp Gln Gln 35	Ser Ala His Ile Ser Pro Ala Ile Pro Val Ile Ile Thr Ala 55	Ser Val Val Phe Val Val Gly Leu Val Gly Asn Ser Leu Val 70 80
Gly	Trp	G1u 45	Ile	Asn
Pro	Ser	Ser	Va1 60	Gly
Asp	Ser	Gly	Pro	Va1 75
Gly 10	Ser	Val	Пе	ren
Arg	Asn 25	Ser	Ala	Gly
Phe	Pro	G1y 40	Pro	Val
Ile	Leu	Asn	Ser 55	Val
Gln	ren -	Ser	Пе	Phe 70
Ile 5	Cys	Asp	His	Val
Pro	Ala 20	Ser	Ala	Val
Ser	Ser	G1u 35	Ser	Ser
Met Glu 1	Ser Pro		Leu Glu 50	
Met 1	Ser	Trp Ala	ren	Val Tyr 65

HUMAN MOUSE	Tyr Ile Phe Asn Leu Ala Leu Ala Asp Ala Leu Val Thr Thr Met Tyr Ile Phe Asn Leu Ala Leu Ala Asp Ala Leu Val Thr Thr Met 100
HUMAN MOUSE	Pro Phe Gln Ser Thr Val Tyr Leu Met Asn Ser Trp Pro Phe Gly Asp Pro Phe Gln Ser Ala Val Tyr Leu Met Asn Ser Trp Pro Phe Gly Asp 125
HUMAN MOUSE	Val Leu Cys Lys Ile Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Val Leu Cys Lys Ile Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr 130
HUMAN	Ser Ile Phe Thr Leu Thr Met Met Ser Val Asp Arg Tyr Ile Ala Val Ser Ile Phe Thr Leu Thr Met Met Ser Val Asp Arg Tyr Ile Ala Val 145
HUMAN	Arg Thr Pro Leu Lys Arg Thr Pro Leu Lys
UMAN MOUSE	I/U Ile Trp Leu Leu Ser Ser Ser Ile Trp Leu Leu Ala Ser Ser

FIG. 4A-2

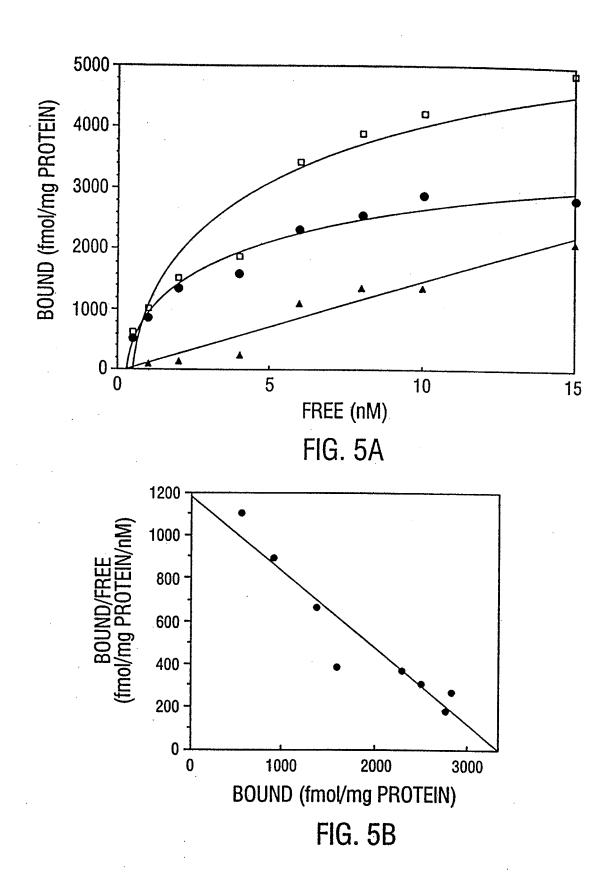
HUMAN	HUMAN	HUMAN	HUMAN	HUMAN
Ala Ala	Glu Glu	Phe Phe 225		Arg
Ala Ile Ala Ile	Glu Cys Glu Cys 210	Met Met	11e 11e 11e 11e	Arg Leu Arg Leu
Val Val	Cys Ser		11e	ren
Leu Leu	Leu	Ile Ile	Ile Val	Ser Ser 260
61 <i>y</i> 61 <i>y</i>	Cys Leu Gln Ser Leu Gln	Lys Ile Cys Lys Ile Cys	Cys Cys 245	G1y G1y
Val Leu Gly Gly Val Leu Gly Gly 195	Phe Phe	Val Val 230	TyT ry	Ser Gly Ser / Ser Gly Ser / 260
Thr Thr	Pro Pro 215	Phe Phe	# F	Arg Arg.
Lys Lys 200	Asp Asp	Ile Val	ren Fen	Arg Glu Arg Glu
Val Val	Asp Asp	Ile Phe Val Phe	Thr Leu Met Thr Leu Met	Lys Lys 265
Lys Val Arg G Lys Val Arg G 200	Asp Asp Asp Tyr Asp Asp Glu Tyr	Ala Ala		Lys Asp NNN / Lys Asp Arg / 265
	Tyr	Phe Phe 235	Leu	NNN Arg
Asp Asp	Ser Ser 220	Val Ile Pro Val Ile Pro	Arg Leu l Arg Leu l	Asn Leu Asn Leu
Val Val 205	Trp Trp	II e	ren Len	Leu
Val Asp V Val Asp V 205	Trp Trp	Pro Pro	Lys Lys	Arg Arg 270
Val Val	Asp Asp	Va) Va)	NNN Ser 255	Arg Arg
11e 11e	Leu	Leu Leu 240	Val Val	I e
Val Ile Val Ile	Trp Trp Asp Leu Trp Trp Asp Leu	Val Leu Val Leu 240		

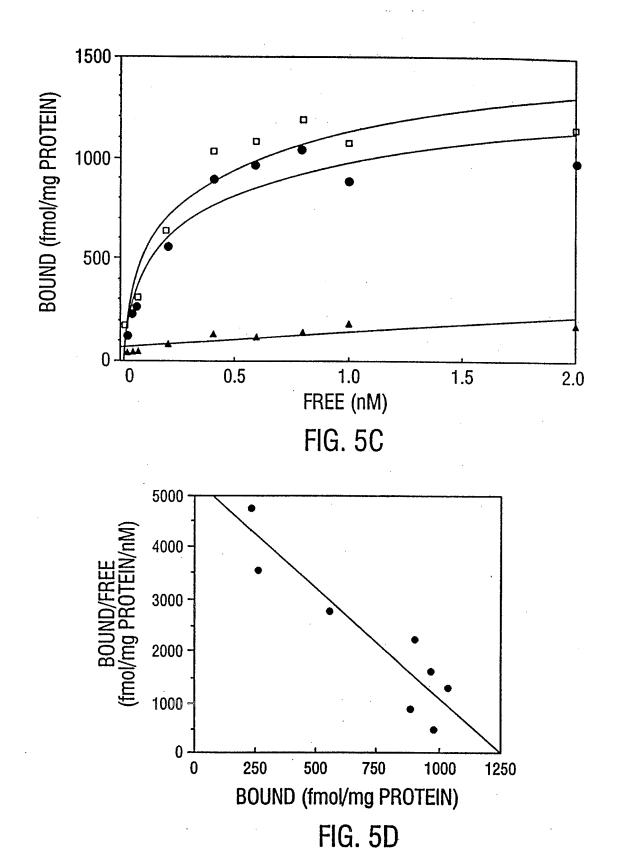
FIG. 4A-3

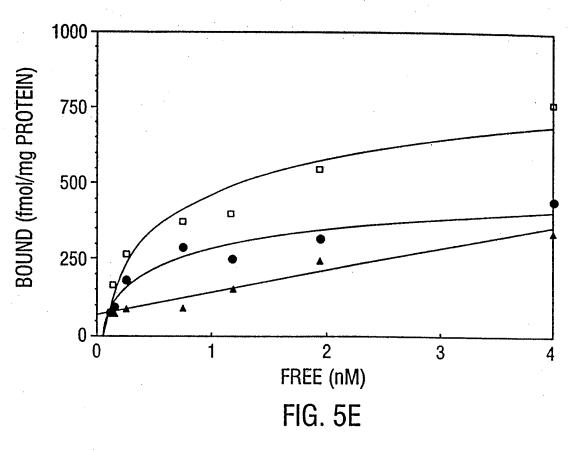
Cys Trp Thr Cys Trp Thr	s s	۲, r 0	בב
dr.	ΞΞ	Tyr Tyr 320	Asn Asn
/s T Trp	Ser His Ser His	6]y 6]y	G]u G]u 335
رې درېs		Cys Ile Ala Leu Gly Cys Ile Ala Leu Gly 315	Phe Leu Asp Glu , Phe Leu Asp Glu , 335
Val Leu Val Val Ala Val Phe Val Val Val Leu Val Val Ala Val Phe Ile Ile 285	u Val Glu Ala Leu Gly Ser T u Val Glu Ala Leu Gly Ser T 300	Ala Ala	ren
Val Ile	G1y G1y 300	II e	Phe Phe
Phe Phe	nə Ten	Cys Cys 315	A1a A1a
Val Val	Ala Ala	he he	Tyr Tyr 330
Ala Ala	G]u G]u	Tyr	Leu
Va1 Va1 280	Val Val	Ty Ty	Ile Val
Val Val	le His Ile Phe Ile Leu Va le His Ile Phe Ile Leu Va 30	Ser Ser Ser Ser 310	Asn Pro Ile Leu 7 Asn Pro Val Leu 7
Val Val	II e	Ser Ser 310	Asn
ren	Phe Phe	Ala Ala Leu Ala Ala Leu	Leu Leu 325
Val Val	Ile Ile	Ala Ala	Ser
Leu Leu 275	His. His	Ala Ala	Ser
Thr Arg Thr Lys	. H H 2	T T T	Asn Asn
Thr	Pro Pro	Ser Ser 305	Thr Asn Thr Asn
HUMAN	HUMAN MOUSE	HUMAN	HUMAN MOUSE

FIG. 4B-1

NNN Met Arg Met	Asp Pro Ala Asp Pro Ala	(SEQ ID NO:12) (SEQ ID NO:2)
Lys Met Lys Met 350	Gln Asp Gln Asp	Val (
Pro Leu l Pro Ile L	Va1 Va1 365	Lys Pro V Lys Pro V 380
Phe Phe	Asn Thr Asn Thr	Asn Asn
Phe Cys Phe Cys 345	Val Arg Val Arg	Met Met Gly Met
Arg Asp Pl Arg Asp Pl	Arg Arg 360	61y 61y 375
Phe Arg Phe Arg	Thr Ser Thr Asn	Ile Asp Asp Val
Cys Cys 340	Ser Ser	G]u Arg
Lys Arg Lys Arg	Arg NNN Arg Gln 355	Leu Arg Ser Met 370
Phe Phe	Glu Arg Glu Arg 355	₹
HUMAN MOUSE	HUMAN MOUSE	HUMAN MOUSE







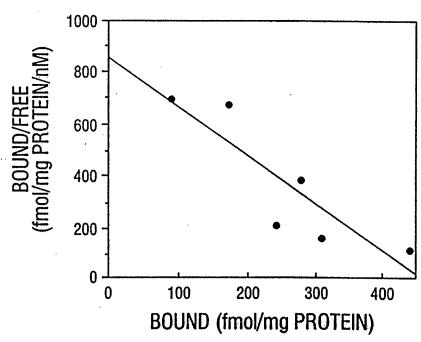
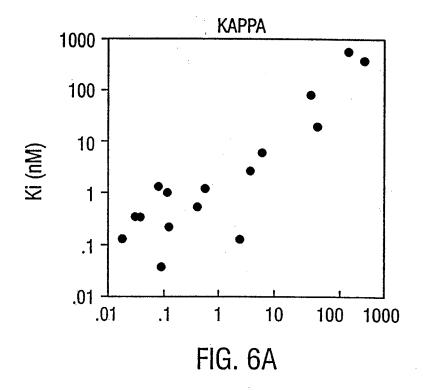
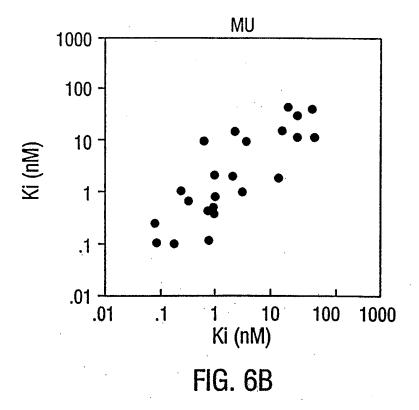


FIG. 5F





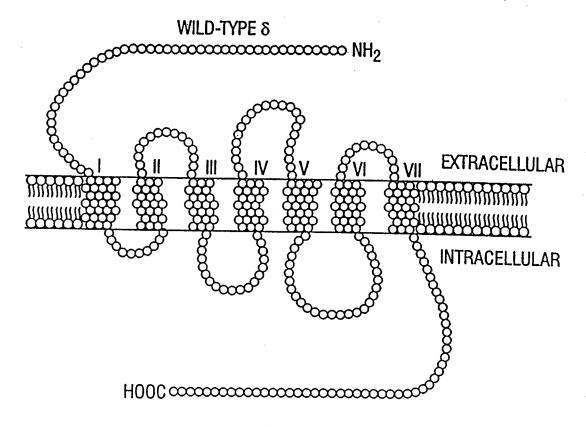


FIG. 7A

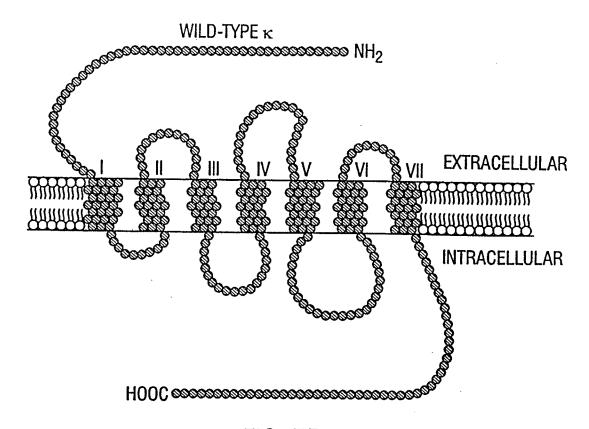


FIG. 7B

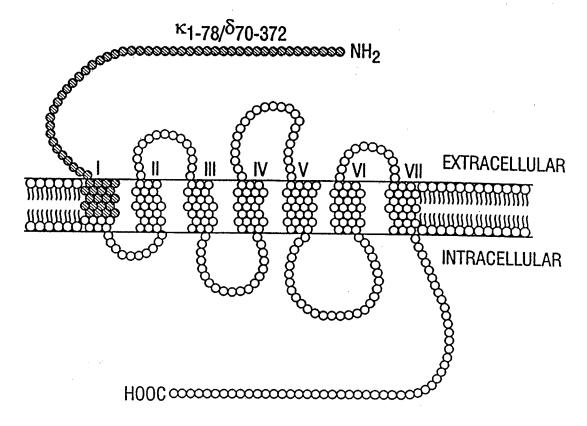


FIG. 7C

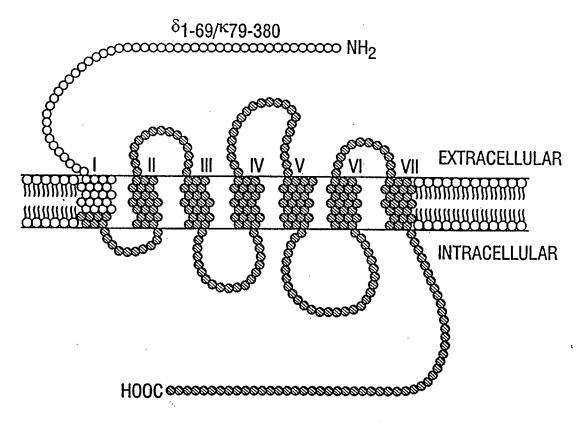


FIG. 7D

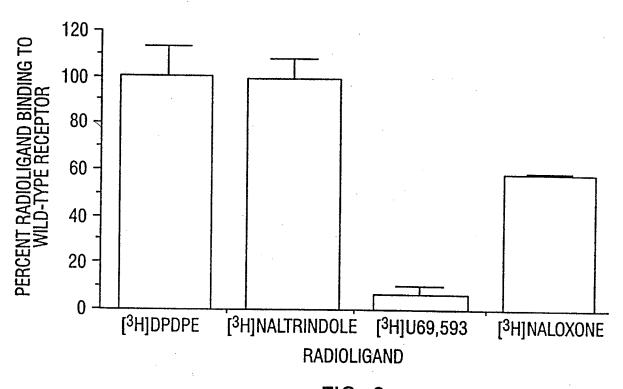


FIG. 8

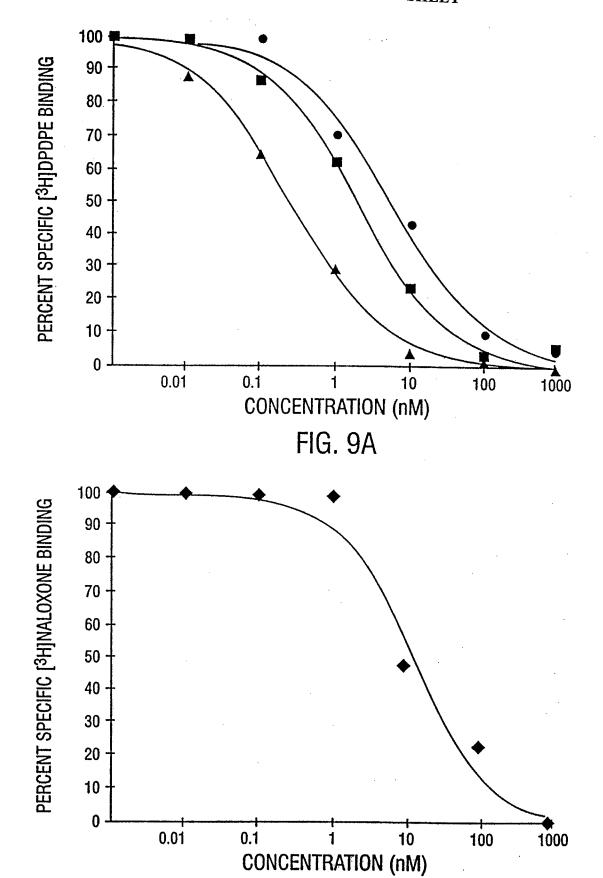


FIG. 9B

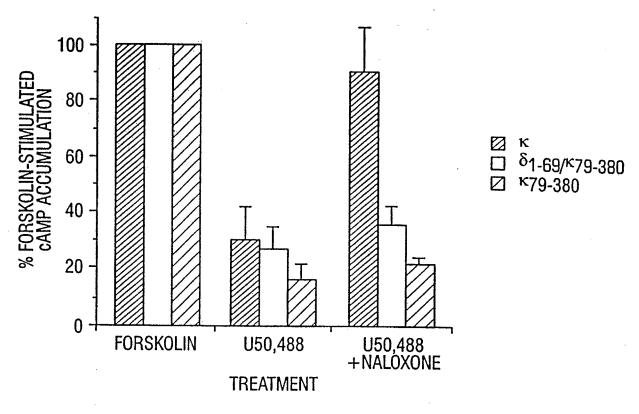
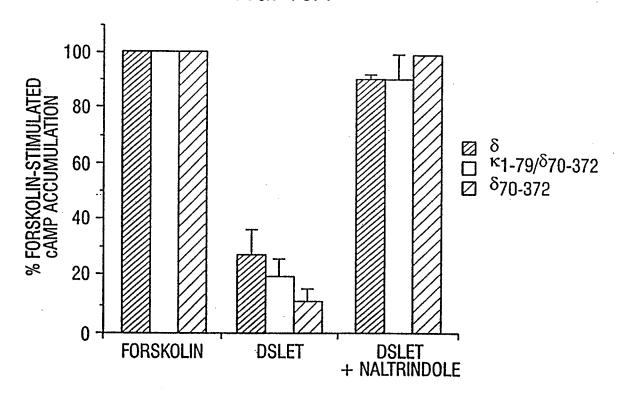
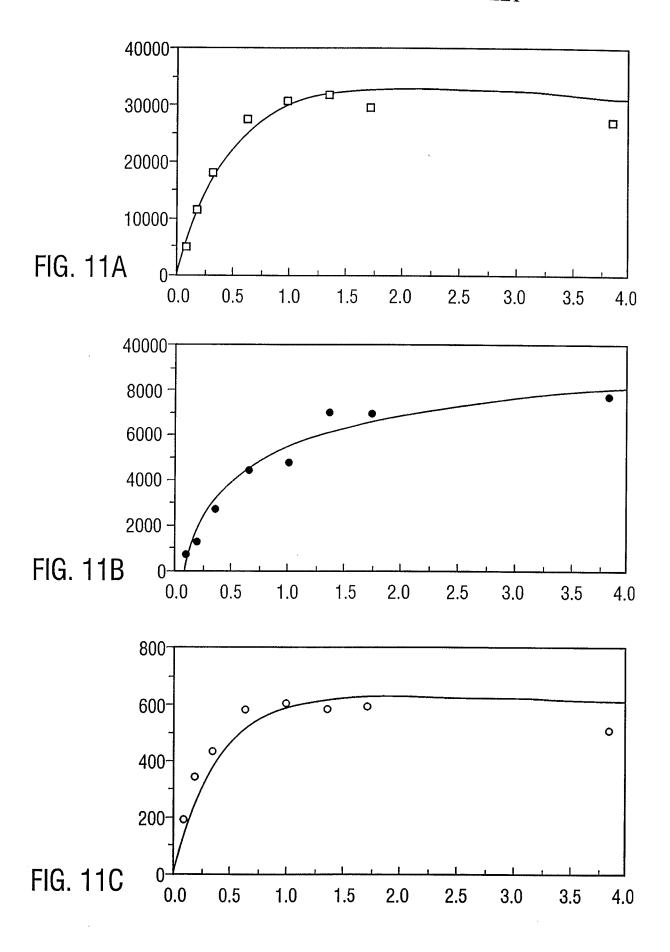
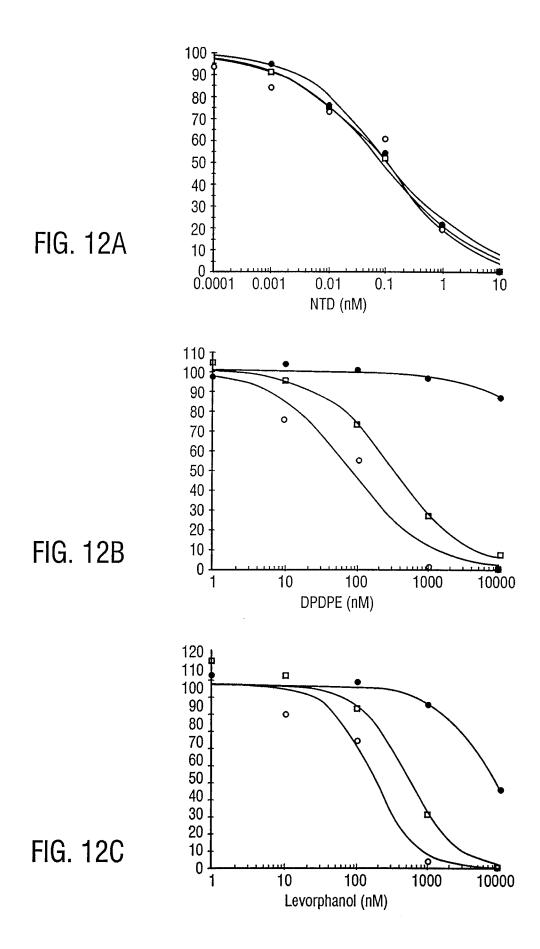


FIG. 10A



TREATMENT FIG. 10B





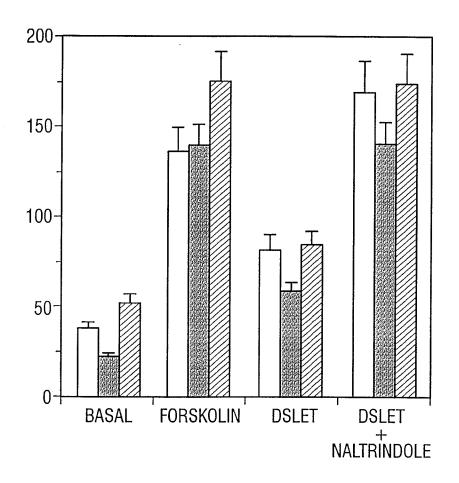
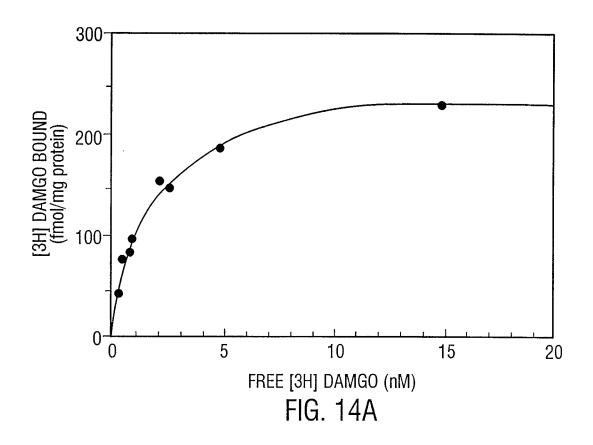
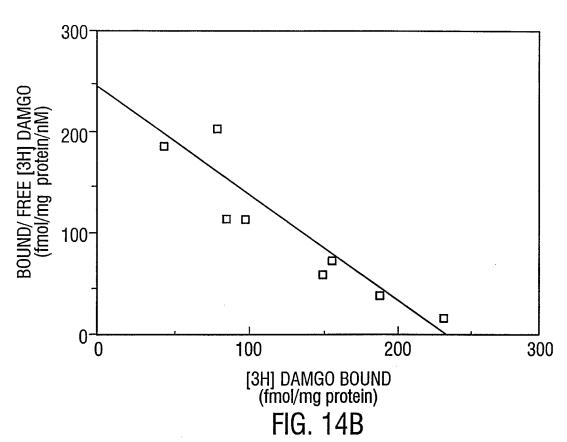
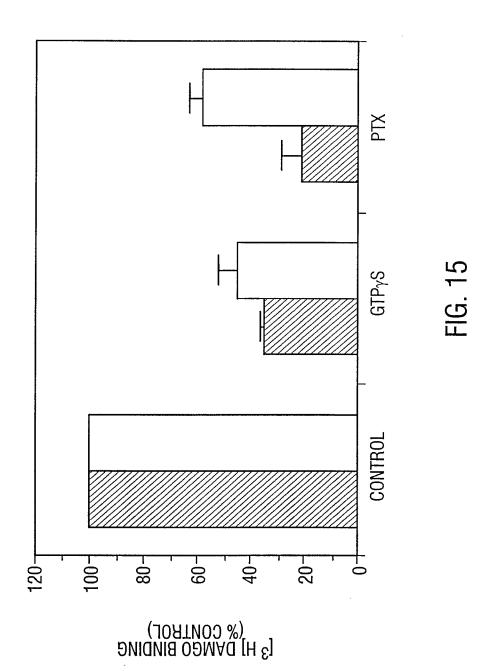
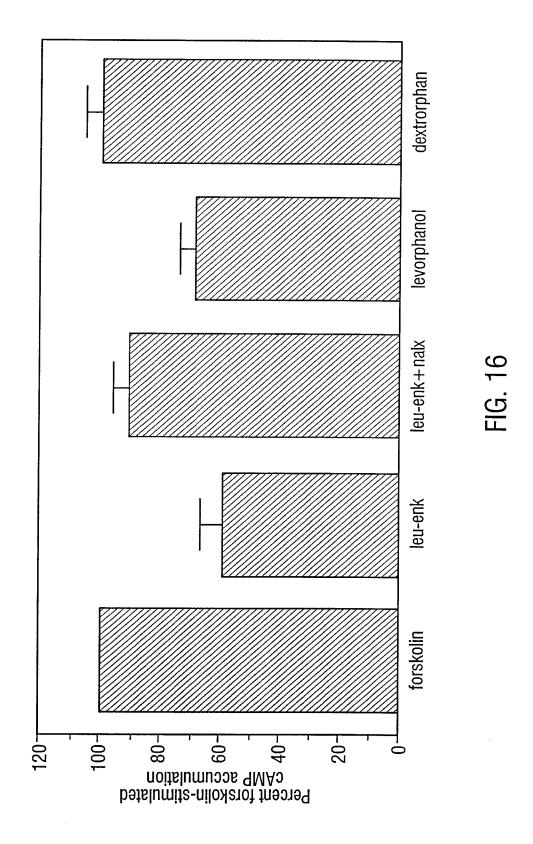


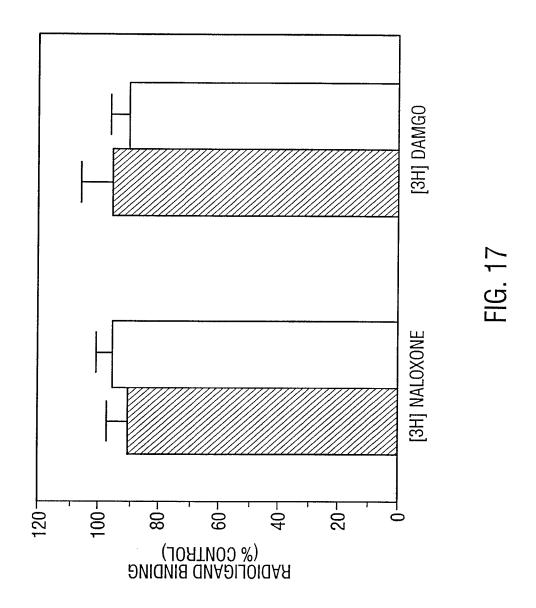
FIG. 13











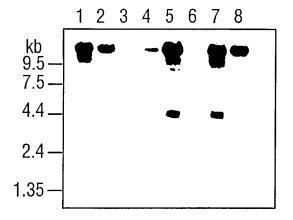


FIG. 18